

TwoSpeciesGrowthDynamics.R

Administrator

Tue Mar 15 14:12:58 2016

```
# Generating growth trajectories for two-species Lotka-Volterra Models
# Parameter list:
```

```
# Time = length of time series
# N_a = vector of population sizes of species A
# N_b = vector of population sizes of species B
# Ka = carrying capacity of species A
# Kb = carrying capacity of species B
# ra = growth rate of species A (constant)
# rb = growth rate of species B (constant)
# N_a0 = initial population size of species A
# N_b0 = initial population size of species B
# alpha = effect of species B on growth of species A
# beta = effect of species A on growth of species B
```

```
LV_Comp <- function (Time=1000,
                      ra=0.1,
                      rb=0.1,
                      N_a0=100,
                      N_b0=100,
                      Ka=400,
                      Kb=200,
                      alpha=0.3,
                      beta=0.6,
                      ret=TRUE){
  N_a <- rep(0,Time) # create vector for N_a
  N_b <- rep(0,Time) # create vector for N_b
  N_a[1] <- N_a0 # initialize N_a
  N_b[1] <- N_b0 # initialize N_b

  for (j in 2:Time){
    dNadt <- ra*N_a[j - 1]*((Ka - N_a[j - 1] - alpha*N_b[j - 1])/Ka)
    dNbdT <- rb*N_b[j - 1]*((Kb - N_b[j - 1] - beta*N_a[j - 1])/Kb)
    N_a[j] <- N_a[j - 1] + dNadt
    N_b[j] <- N_b[j - 1] + dNbdT
  }

  m <- cbind(seq(1,Time),N_a,N_b)
  matplot(x=m[,1],y=m[,c(2,3)],
          type="l",
          lty=1,
          xlab="Time",
          ylab="N",
          ylim=c(0,max(m[, -1])))

  if(ret==TRUE) return(m)
```

```
}  
LV_Comp(ret=FALSE)
```

